

Fig. 1

IDENTIFIED LAB mRNA SEQUENCES

CGGGAGCTTGAAGGACACAAGAATGGGAGGAAAGGCGGACTCTCAGGAAC (Ribosome Binding Site)
 TTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACAT (Start Codon)
CTGTAGCTGTCGTTTGGTTGATCTTGTTGACTATGAGGAAGTTCTAGGA
AAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGTGTGGATGA
TGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAG
TCCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCCGAGGAGCAGGTTCCCT
GTGGAGGCAGAACCCAGAAATATCGAAGATGAAGCAAAAGAACAATTCA
GTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACT
TGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAG
TTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGA
AGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTT
CACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAAT
CCAGATTCCAGTGAACCACTAGTAGAAGATGAAAGATTGCACCATGATAC
AGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTC
TAGAAAATGAAGGGATAGAAAATCACAGAAGTAACTGCTCCCCCTGAGGAT
AATCCTGTAGAAGATTACAGGTAATTGTAGAAGAAGTAAGCATTTTTCC
TGTGGAAGAACAGCAGGAAGTACCACCAGATACTTAAAGCTTCAAAAAGA (Stop Codon)
 CTGCCCCTACCACCACAGGAGGACCAGCCTAACCATACGCTCCAAAAGAT
 GGCTGTGATAGATCTTGTGAAGCAATTACTGAGCAGATCAAGATCTTTGG
 GAAGGAACACTAAAGATGTTTGAATGAATTATAGTCCACTGGCATTTTA
 GTGTATTTTTTTTTCTTTTGTAGAAACACACATTTCTAAAAATGTCATGTT
 ACATTCTGCATGTCCCTTTTGATAGCATTAGTGGATCCATTGGATTCTT
 TTTTCTTTTTGTGAGACAGCTTTTAGTCTTACCTGAATTTATGTGTGTT (Instability Sequence)
 TTTCCGACAGTGGTTAATAATTATATTGGTGATGTAGCAGCAATTGTGTT
 GGCAGGGTTTTATATATTATAGTAATTAACACTAACTGTTGGACTGAC
 TTGTGTACACTGTGTTAAACATGATTTAAAGCTATTAAGAGTACTTTGT (Instability Sequence)
 GTTAGCACTCTTAAAAACGCTAACAGAGATCATCATTAGCTGTGAAGATT
 TGAGTTGTATATACCTGCACTGATATTCTTATCAAAAATTTCTACATTAG
 CTTTAAGTGTTCAGATTAACACTTTTGAAACCTTTGTAGCTTTTAGCTGA
 TTAATTAGAAAAATTAATATTTTCAGTGAAAGTTTTAAATTATCATTTATT (Instability Sequence)
 TATTTTTTTTAAATGAGAGGGGAAAGCTGAAATTCCTTGTAAAGACACAAG
 GAAAAAGAATGGCCCTACTATTATCATGCAAAAATGCTTTGTTGGCACCT
 CAGATTAATCATATAATAGCTATAGTCTCTCAGCATTGTGTTAAATTTT
 AGAAAACCTGTATAAATTACTGGTGCATAACTTAAAGATTATTCTGCCTT
 TGGCTAATTGAGTAATTCCTCCAGCACTAGAGACCGCTCAGTGCTCTT
 ACTAGATGAATCAGTAACGCCTTGAGCTGGGTTGATTGAGGATGTGTGA
 AAAAGCTCACAGAGCCCGATGCCTGCTGCTATTTACGGCAATGAGCCTT
 TTTCTTTCTACACTGAAGATTTTCTTCTTATTTAATGTGGTTATTTTGG (Instability Sequence)
 GCTCAGAAATAATTGCTCTGTTGAAAATAATCCTTTGTCAGAAAAGAAGG
 TAGCTACCACATCATTTTGAAGGACCATGAGCAACTATAAGCAAAGCCA
 TAAGAAGTGGTTTGATCGATATATTAGGGGTAGCTCTTGATTTTGTTAAC
 ATTAAGATAAGGTGACTTTTTCCCCCTGCTTTTAGGATTAATAATCAAAGA (Sub-optimal Poly-
 adenylation Site)
 TACTTCTATATTTTATCACTATAGATCATAGTTATTATACAATGTAGTG
 AGTCCTGCATGGGTACTCGATGTGTAATGAAACCTGAAATAATAATAAGA
 TAATAAGAAAAGCAATAATTTTCTAAAGCTGTGCTGTCGGTGATACAGAG
 ATGATACTCAAATTATAATAAACTCTTCATTTTGTGAATTATAGAAGCT (Optimal Polyadeny-
 lation Site)
 ACTTTTTATAAAGCCATATTTTTTTAGGGAACTAAGGAGTGACATAGAA
 CTGATGAATGAGTAAAGTAAGTTTTGCTGGATTTTTGTAGAAGTCTGGA
 CGTTGAGGATTCATTATGCTGTGGTTAACTTTAAATATTTTT

Fig. 2

COMPUTER PREDICTED DOMAINS
IN LABYRINTHIN

MVIALGVWTSVAVVWFDLVDDYEEVLGKLGGIYDADGDGDFDVDDAKVLLGLK

^

ERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNI~~EDEAKEQIQSLLHEMVHAE~~

HVEGEDLQQEDGPTGEPQQEDDEF~~LMATDVDDRFETLEPEVSHEETEHSYHV~~

EETVSQDCNQDMEEMMSEQENPDSSEP~~VVEDERLHHD~~TDDvtyqvyeegavY
 <--MAD I-->

EPLENEGIEITEVTAPEDNPVEDSQviveevsifpvEEQWCP~~PDT~~
 ^ <--MAD II-->

____ Predicted Ca⁺⁺ Binding Region

VLGKLGGIYDADGDGDFDVDDAKVLLGLK

Parvalbumin
 Calmodulin
 Troponin-C

vkafaiidqdksgfiedelklflqnf
 fkeafslfdkdgdgtittkelgtvmrsl
 ladcfrvfdknadgfidieelgeilrat

Ca⁺⁺ Binding Residues
 Required Residue

* * * * *
 +

SYMBOL KEY

BOLD = eukaryotic Leader Sequence

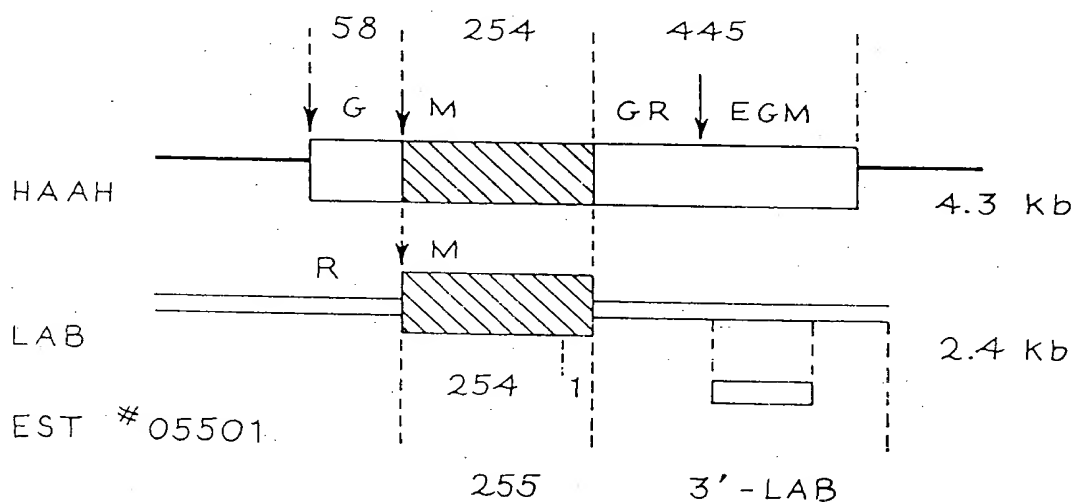
_____ = Myristylation site

^

lower case = Membrane Anchoring Domain (MAD)

<----->

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↓ = START CODON
 R = RIBOSOME BINDING SITE
 E = ENZYMATIC SITE
 G = GLYCOSYLATION SITE
 M = MEMBRANE ANCHORING DOMAIN
 3'-LAB = CONTAINS POLY A SIGNAL (x2);
 INSTABILITY SEQUENCE (x4)

Fig. 3